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SEQUENCE LISTING

<110> Gurney, Mark  
Bienkowski, Michael J.

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<150> 60/169,232

<151> 1999-12-06

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Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile		
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Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
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His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
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Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
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Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
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His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
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Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val	195	200	205
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Ala	Gln	Ile	Arg	Ser	Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu	450	455	460
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Glu	Glu	Ile	Gln	Asp	Glu	Val	Asp	Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn	485	490	495
Tyr	Ser	Asp	Asp	Val	Leu	Ala	Asn	Met	Ile	Ser	Glu	Pro	Arg	Ile	Ser	500	505	510







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Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
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Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
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His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
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Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
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Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
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Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
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Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
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Asn Met Leu Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
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Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
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Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
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Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
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Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
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Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
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Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
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Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
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Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
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<211> 697  
<212> PRT  
<213> Homo sapiens

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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
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Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
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Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
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Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95  
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110  
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125  
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
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Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
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Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
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Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
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Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
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Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
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Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240  
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255  
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
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002050 4483550

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Thr	Arg	Pro	Gly	Ser	Gly	Leu	Thr	Asn	Ile	Lys	Thr	Glu	Glu	Ile	Ser
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His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
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Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
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Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
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Phe Phe Glu Gln Met Gln Asn Lys Lys  
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<210> 19  
<211> 2094  
<212> DNA  
<213> Homo sapiens

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<210> 20  
<211> 697

<213> Homo sapiens

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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
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Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
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Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
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Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
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Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu.  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
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Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
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Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly
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Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser
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Ala	Pro	His	Pro 100	Phe	Leu	His	Arg	Tyr 105	Tyr	Gln	Arg	Gln	Leu 110	Ser	Ser
Thr	Tyr	Arg 115	Asp	Leu	Arg	Lys	Gly 120	Val	Tyr	Val	Pro	Tyr 125	Thr	Gln	Gly
Lys	Trp 130	Glu	Gly	Glu	Leu	Gly 135	Thr	Asp	Leu	Val	Ser 140	Ile	Pro	His	Gly
Pro 145	Asn	Val	Thr	Val	Arg 150	Ala	Asn	Ile	Ala	Ala 155	Ile	Thr	Glu	Ser	Asp 160
Lys	Phe	Phe	Ile	Asn 165	Gly	Ser	Asn	Trp	Glu 170	Gly	Ile	Leu	Gly	Leu 175	Ala
Tyr	Ala	Glu	Ile 180	Ala	Arg	Pro	Asp	Asp 185	Ser	Leu	Glu	Pro	Phe 190	Phe	Asp
Ser	Leu	Val 195	Lys	Gln	Thr	His	Val 200	Pro	Asn	Leu	Phe	Ser 205	Leu	His	Leu
Cys	Gly 210	Ala	Gly	Phe	Pro	Leu 215	Asn	Gln	Ser	Glu 220	Val	Leu	Ala	Ser	Val
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Ser	Leu	Trp	Tyr 245	Thr	Pro	Ile	Arg	Arg	Glu 250	Trp	Tyr	Tyr	Glu	Val 255	Ile
Ile	Val	Arg	Val 260	Glu	Ile	Asn	Gly	Gln 265	Asp	Leu	Lys	Met	Asp 270	Cys	Lys
Glu	Tyr	Asn 275	Tyr	Asp	Lys	Ser	Ile 280	Val	Asp	Ser	Gly 285	Thr	Thr	Asn	Leu
Arg	Leu 290	Pro	Lys	Lys	Val	Phe 295	Glu	Ala	Ala	Val	Lys 300	Ser	Ile	Lys	Ala
Ala 305	Ser	Ser	Thr	Glu	Lys 310	Phe	Pro	Asp	Gly	Phe 315	Trp	Leu	Gly	Glu	Gln 320
Leu	Val	Cys	Trp	Gln 325	Ala	Gly	Thr	Thr	Pro 330	Trp	Asn	Ile	Phe	Pro 335	Val
Ile	Ser	Leu	Tyr 340	Leu	Met	Gly	Glu	Val 345	Thr	Asn	Gln	Ser	Phe 350	Arg	Ile
Thr	Ile	Leu 355	Pro	Gln	Gln	Tyr	Leu 360	Arg	Pro	Val	Glu	Asp 365	Val	Ala	Thr
Ser	Gln 370	Asp	Asp	Cys	Tyr	Lys 375	Phe	Ala	Ile	Ser	Gln 380	Ser	Ser	Thr	Gly
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			20					25					30			
Arg	Leu	Pro	Leu	Arg	Ser	Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	
		35					40					45				
Leu	Pro	Arg	Glu	Thr	Asp	Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	
	50					55					60					
Ser	Phe	Val	Glu	Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	
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Tyr	Tyr	Val	Glu	Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	
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<210> 26
<211> 433
<212> PRT
<213> Homo sapiens
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Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg
          35          40          45

Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro
  50          55          60

Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala
  65          70          75          80

Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln
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Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr
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<400> 27						
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      35          40          45

Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val
  50          55          60

Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe
  65          70          75          80

Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu
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Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu
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Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val
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Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn
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<210> 30  
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 <212> PRT  
 <213> Homo sapiens

<400> 30

Met	Ala	Gln	Ala	Leu	Pro	Trp	Leu	Leu	Leu	Trp	Met	Gly	Ala	Gly	Val
1				5					10					15	
Leu	Pro	Ala	His	Gly	Thr	Gln	His	Gly	Ile	Arg	Leu	Pro	Leu	Arg	Ser
			20					25					30		
Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp
		35					40					45			
Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val
	50					55					60				
Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr
65					70					75					80
Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser
				85					90					95	
Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr
			100					105					110		
Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val
	115						120					125			
Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp
	130					135					140				
Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile
145					150					155					160
Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp
				165					170						175

F00050-42950

```
<210> 31
<211> 1380
<212> DNA
<213> Homo sapiens

<400> 31
atggcccaag ccctgccctg gctcctgctg tggatgggcg cgggagtgtc gcctgcccac 60
```

```
<210> 32
<211> 459
<212> PRT
<213> Homo sapiens
```

<400>	32															
Met	Ala	Gln	Ala	Leu	Pro	Trp	Leu	Leu	Leu	Trp	Met	Gly	Ala	Gly	Val	
1				5					10					15		
Leu	Pro	Ala	His	Gly	Thr	Gln	His	Gly	Ile	Arg	Leu	Pro	Leu	Arg	Ser	
			20					25					30			
Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp	
		35					40					45				
Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val	
	50					55					60					
Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr	
65					70					75					80	
Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser	
				85					90					95		
Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr	
			100					105					110			
Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val	
		115					120					125				
Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp	
	130					135					140					
Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	
145					150					155					160	
Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp	
				165					170					175		



```
<400> 39
cggcatccgg ctgccctgc gtacgggtct ggggtggtgct ccaactgggtc tgcgtctgcc 60
ccgggaqacc gacqaag                                     77
```

<210> 40  
<211> 77  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hu-Asp2

<400> 40  
cttcgtcggg ctcccggggc agacgcagac ccagtggagc accacccaga ccgctacgca 60  
ggggcagccg gatgccg 77

<210> 41  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Caspase 8  
Cleavage Site

<400> 41  
gatcgatgac tatctctgac tctccgctgg actctggtat cgaaaccgac g 51

<210> 42  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Caspase 8  
Cleavage Site

<400> 42  
gatccgctcg tttcgatacc agagtccagc ggagagtcag agatagtcac c 51

<210> 43  
<211> 32  
<212> DNA  
<213> Homo sapiens

<400> 43  
aaggatcctt tgtggagatg gtggacaacc tg 32

<210> 44  
<211> 36  
<212> DNA  
<213> Homo sapiens

<400> 44  
gaaagctttc atgactcatc tgtctgtgga atgttg 36

<210> 45  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: 6-His tag

<400> 45  
gatcgcatca tcaccatcac catg 24

<210> 46  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: 6-His tag

<400> 46  
gatccatggt gatggtgatg atgc 24

<210> 47  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 47  
gactgaccac tgcaccaggt tc 22

<210> 48  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 48  
cgaattaaat tccagcacac tggctacttc ttgttctgca tctcaaagaa c 51

<210> 49  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 49  
cgaattaaat tccagcacac tggcta 26

<210> 50  
<211> 1287  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hu-Asp2(b)  
delta TM

<400> 50  
atggcccaag ccctgccctg gctcctgctg tggatgggag cgggagtgct gcctgcccac 60  
ggcaccagc acggcatccg gctgcccctg cgcagcggcc tggggggcgc cccctctggg 120  
ctgaggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180  
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240  
gtgggcagcc cccgcagac gctcaacatc ctggtggata caggcagcag taactttgca 300  
gtgggtgctg cccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 360  
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420  
ctgggcaccg acctggtaag catccccat ggcccccaacg tcaactgtgc tgccaacatt 480  
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcacacct 540

```
<210> 51
<211> 428
<212> PRT
<213> Artificial Sequence
```

<400>	51																
Met	Ala	Gln	Ala	Leu	Pro	Trp	Leu	Leu	Leu	Trp	Met	Gly	Ala	Gly	Val		
1				5					10					15			
Leu	Pro	Ala	His	Gly	Thr	Gln	His	Gly	Ile	Arg	Leu	Pro	Leu	Arg	Ser		
			20					25					30				
Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp		
		35					40					45					
Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val		
	50					55					60						
Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr		
65					70					75					80		
Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser		
				85					90					95			
Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr		
			100					105					110				
Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val		
		115					120					125					
Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp		
	130					135					140						
Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile		
145					150					155					160		
Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp		
				165					170					175			
Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Leu	Cys	Gly		
			180					185					190				
Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly		
		195					200					205					

```
<210> 52
<211> 1305
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hu-Asp2(b)
      delta TM
```

<400> 52						
atggcccaag	ccctgccctg	gctcctgctg	tggatgggcg	cgggagtgt	gcctgccac	60
ggcaaccagc	acggcatccg	gctgcccctg	cgcagcggcc	tggggggcgc	ccccctgggg	120
ctgcggtctg	cccgggagac	cgacyaagag	cccgaggagc	ccggccggag	gggcagcttt	180
gtggagatgc	tggacaacct	gaggggcaag	tcggggcagg	gctactacgt	ggagatgacc	240
gtggcgagcc	ccccgcagac	gctcaacatc	ctgggtggata	caggcagcag	taactttgca	300
gtgggtgctg	ccccccaccc	cttcctgcat	cgtactacc	agaggcagct	gtccagcaca	360
taccgggacc	tccggaagg	tgtgtatgtg	ccctacaccc	agggcaagt	ggaaggggag	420
ctgggcaccg	acctggtaag	catccccct	ggcccccaacg	tcactgtgcy	tgccaacatt	480
gtgcctatca	ctgaatcaga	caagttcttc	atcaacggt	ccaactggga	aggcatcctg	540
gggtctggcct	atgctgagat	tgccaggctt	tgtgggtctg	gcttccccct	caaccagtct	600

```

gaagtgtctgg cctctgtcgg agggagcatg atcattggag gtatcgacca ctcgctgtac 660
acaggcagtc tctggtatac acccatccgg cgggagtggt attatgaggt catcattgtg 720
cgggtggaga tcaatggaca ggatctgaaa atggactgca aggagtacaa ctatgacaag 780
agcattgtgg acagtggcac caccaacctt cgtttgcca agaaagtgtt tgaagctgca 840
gtcaaatacca tcaaggcagc ctctccacag gagaagtcc ctgatgggtt ctggctagga 900
gagcagctgg tgtgtctggca agcaggcacc accccttgga acattttccc agtcattctca 960
ctctaccta tgggtgaggt taccaaccag tccttccgca tcaccatcct tccgcagcaa 1020
tacctgcggc cagtgggaaga tgtggccacg tcccaagacg actgttataa gtttgccatc 1080
tcacagtcac ccacgggcac tgttatggga gctgttatca tggagggctt ctacgttgct 1140
tttgatcggg cccgaaaacg aattggcttt gctgtcagcg cttgccatgt gcacgatgag 1200
ttcaggacgg cagcgggtgga aggcctttt gtcaccttgg acatggaaga ctgtggctac 1260
aacattccac agacagatga gtcacagcag cagcagcagc agtga 1305

```

<210> 53

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hu-Asp2(b)  
delta TM

<400> 53

```

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1           5           10           15
Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
          20          25          30
Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
          35          40          45
Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
          50          55          60
Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
          65          70          75          80
Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
          85          90          95
Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
          100         105         110
Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
          115         120         125
Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
          130         135         140
Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
          145         150         155         160
Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
          165         170         175
Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
          180         185         190
Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
          195         200         205

```

102050-475550

<400> 54						
atgctgcccgc	gtttggcact	gctcctgctg	gccgcctgga	cggtctcgggc	gctggaggtta	60
cccactgatg	gtaatgctgg	cctgctggct	gaaccccaga	ttgccatgtt	ctgtggcaga	120
ctgaacattg	acatgaatgt	ccagaatggg	aagtgggatt	catagccatc	agggaccaa	180
acctgcattg	ataccaaagga	agccatcctg	cagtatgtgc	aagaagtcta	ccctgaactg	240
cagatcacca	atgtggtaga	agccaaccaa	ccagtaccca	tcagaaactg	gtgcaagcgg	300
ggccgcaagc	agtgcaagac	ccatccccac	tttgtgattc	cctaccgctg	cttagt.tgg	360
gagtttgtaa	gtgatgccct	tctcgttcct	gacaagtgca	aattcttaca	ccaggagagg	420
atggatgttt	gcgaaactca	tcttcactgg	cacaccgtcg	ccaaagagac	atgcagttag	480
aagagtacca	acttgcata	ctacggcatg	ttgctgccct	gcggaattga	caagttccga	540
ggggtagagt	tttgtgtgtg	cccactggct	gaagaaagtg	acaatttgga	ttctgctgat	600

```
<210> 55
<211> 770
<212> PRT
<213> Homo sapiens
```

<400>	55															
Met	Leu	Pro	Gly	Leu	Ala	Leu	Leu	Leu	Leu	Ala	Ala	Trp	Thr	Ala	Arg	
1				5					10					15		
Ala	Leu	Glu	Val	Pro	Thr	Asp	Gly	Asn	Ala	Gly	Leu	Leu	Ala	Glu	Pro	
			20					25					30			
Gln	Ile	Ala	Met	Phe	Cys	Gly	Arg	Leu	Asn	Met	His	Met	Asn	Val	Gln	
		35					40					45				
Asn	Gly	Lys	Trp	Asp	Ser	Asp	Pro	Ser	Gly	Thr	Lys	Thr	Cys	Ile	Asp	
	50					55					60					
Thr	Lys	Glu	Gly	Ile	Leu	Gln	Tyr	Cys	Gln	Glu	Val	Tyr	Pro	Glu	Leu	
65					70					75					80	
Gln	Ile	Thr	Asn	Val	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn	
				85					90					95		
Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val	
			100					105					110			
Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu	
		115					120					125				
Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys	
	130					135					140					



```
<210> 56
<211> 2253
<212> DNA
<213> Homo sapiens
```

atgctgcccc	gtttggcact	gtcctctgtg	gccgcctgga	cggctcgggc	gctggaggtg	60
cccactgatg	gtaatgctgg	cctgctgggt	gaaccccaga	ttgccatgtt	ctgtggcaga	120
ctgaacatgc	acatgaatgt	ccagaatggg	aagtgggatt	cagatccatc	agggaccaa	180
acctgcattg	ataccaagga	aggcatcctg	cagtattgcc	aagaagtcta	ccctgaactg	240
cagatcacca	atgtggtaga	agccaaacca	ccagtgarca	tccagaactg	gtgcgaagcg	300
ggcgcgaagc	agtgcgaagc	ccatccccac	ttagtgattc	cctaccgctg	cttagttggt	360
gagtttgtaa	gtgatgcctt	tctcgttctt	gacaaagtgca	aattctttaca	ccaggagagg	420
atggatgttt	gcgaaactca	tcttcaactg	cacaccgtcg	ccaagagagc	atgcagttag	480
aagagtacca	acttgcatga	ctacggcatg	ttgctgccct	gcggaattga	caagttccga	540
ggggtagagt	ttgtgtgttg	cccactgggt	gaagaaaagt	acaatgtgga	ttctgctgat	600
gcggaggagg	atgactcgga	tgtctgggtg	ggcggagcag	acacagacta	tgcagatggg	660
agtgaagaca	aagttagtga	agtagcagag	gaggaagaag	tggctgaggt	ggaagaagaa	720
gaagccgatg	atgacgagga	cgttaggagg	gtgtgatgag	tagaggaaaga	ggctgaggaa	780
ccctacgaag	aagccacaga	gagaaccacc	agcattgcca	ccaccaccac	caccaccaca	840
gagtctgtgg	aagaggtggt	tcgagaggtg	tgctctgaac	aagccgagac	ggggccgtgc	900
cgagcaatga	tctcccgtcg	gtactttgat	gtgactgaag	ggaagtgtgc	ccattctttt	960
tacggcggat	gtggcggcaa	ccggaacaac	tttgacacag	aagagtactg	catggccgtg	1020
tgtggcagcg	ccattctctac	acagcagccc	agtacccctg	atgccgttga	caagtatctc	1080
gagacacctg	gggatgagaa	tgaacctgcc	catttccaga	aagccaaaga	gaggtcttag	1140
gccaagcacc	gagagagaat	gtcccaggtc	atgagagaat	gggaagagyc	agaacgtcaa	1200
gcaaagaact	tgcctaaagc	tgataagaag	gcagttatcc	agcatttcca	ggagaaagtg	1260
gaatcttttg	aacaggaagc	agccaacgag	agacagcagc	tggtagagac	acacatggcc	1320
agagtggaag	ccatgctcaa	tgaccgcgcg	cgcttggccc	tggagaacta	catcaccgct	1380
ctgcaggttg	ttctctctcg	gcctcgtcac	gtgttcaata	tgttaaagaa	gtatgtccgc	1440
gcagaacaga	aggacagaca	gcacacccta	aagcattttcg	agcatgtgcg	catgttggtat	1500
cccaagaaaq	ccgctcagat	ccggtcccag	gttatgavac	acctcgtgtg	gatttttagag	1560
cgcatgaatc	agtctctctc	cctgctctac	aacgtgcctg	cagtggccga	gyagattcag	1620
gatgaagtgg	atgagctgct	tcagaaagag	caaaactatt	cagatgacgt	cttggccaac	1680
atgattagtg	aaccaaggat	cagttacgga	aacgatgtct	tcatgccatc	tttgaccgaa	1740
acgaaaacca	ccgtggagct	ccttcccgtg	aatggagagt	tcagccttga	cgatctccag	1800
ccgtggcatt	cttttggggc	tgactctgtg	ccagccaaca	cagaaaacga	agttgagcct	1860
gttgatgcc	gccctgtctg	cgaccgagga	ctgaccactc	gaccaggttc	tgggtttgaca	1920
aatatcaaga	cggaggagat	ctctgaagtg	aagatggatg	cagaattccg	acatgactca	1980
ggatatgaag	ttcatcatca	aaaattgggtg	ttctttgcag	aagatgtggg	ttcaaacaaa	2040
ggtgcaatca	ttggactcat	ggtggggcgt	gttgtcatag	cgacagtgat	cgtcatcacc	2100
ttggtgatgc	tgaagaagaa	acagtacaca	tccatttcac	atggtgtggt	ggaggttgac	2160
gccgctgtca	ccccagagga	gcgccacctg	tccaagatgc	agcagaacgg	ctacgaaaat	2220
ccaacctaca	agttcttttga	qcaqatqcaq	aac			2253

<213> Homo sapiens

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
 85 90 95  
 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
 100 105 110  
 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
 115 120 125  
 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
 130 135 140  
 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
 145 150 155 160  
 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
 165 170 175  
 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
 180 185 190  
 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
 195 200 205  
 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
 210 215 220  
 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
 225 230 235 240  
 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
 245 250 255  
 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
 260 265 270  
 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
 275 280 285  
 Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
 290 295 300  
 Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
 305 310 315 320  
 Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
 325 330 335  
 Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr  
 340 345 350  
 Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu  
 355 360 365  
 His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg  
 370 375 380  
 Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln  
 385 390 395 400  
 Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe  
 405 410 415

Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	Gln	Glu	Ala	Ala	Asn	Glu	Arg	Gln
			420					425					430		
Gln	Leu	Val	Glu	Thr	His	Met	Ala	Arg	Val	Glu	Ala	Met	Leu	Asn	Asp
		435					440					445			
Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	Tyr	Ile	Thr	Ala	Leu	Gln	Ala	Val
	450					455					460				
Pro	Pro	Arg	Pro	Arg	His	Val	Phe	Asn	Met	Leu	Lys	Lys	Tyr	Val	Arg
465					470					475					480
Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	Thr	Leu	Lys	His	Phe	Glu	His	Val
				485					490					495	
Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	Ala	Gln	Ile	Arg	Ser	Gln	Val	Met
			500					505					510		
Thr	His	Leu	Arg	Val	Ile	Tyr	Glu	Arg	Met	Asn	Gln	Ser	Leu	Ser	Leu
		515					520					525			
Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala	Glu	Glu	Ile	Gln	Asp	Glu	Val	Asp
	530					535					540				
Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn	Tyr	Ser	Asp	Asp	Val	Leu	Ala	Asn
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Met	Ile	Ser	Glu	Pro	Arg	Ile	Ser	Tyr	Gly	Asn	Asp	Ala	Leu	Met	Pro
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Ser	Leu	Thr	Glu	Thr	Lys	Thr	Thr	Val	Glu	Leu	Leu	Pro	Val	Asn	Gly
			580					585					590		
Glu	Phe	Ser	Leu	Asp	Asp	Leu	Gln	Pro	Trp	His	Ser	Phe	Gly	Ala	Asp
		595					600					605			
Ser	Val	Pro	Ala	Asn	Thr	Glu	Asn	Glu	Val	Glu	Pro	Val	Asp	Ala	Arg
	610					615					620				
Pro	Ala	Ala	Asp	Arg	Gly	Leu	Thr	Thr	Arg	Pro	Gly	Ser	Gly	Leu	Thr
625					630					635					640
Asn	Ile	Lys	Thr	Glu	Glu	Ile	Ser	Glu	Val	Lys	Met	Asp	Ala	Glu	Phe
				645					650					655	
Arg	His	Asp	Ser	Gly	Tyr	Glu	Val	His	His	Gln	Lys	Leu	Val	Phe	Phe
			660					665					670		
Ala	Glu	Asp	Val	Gly	Ser	Asn	Lys	Gly	Ala	Ile	Ile	Gly	Leu	Met	Val
		675					680					685			
Gly	Gly	Val	Val	Ile	Ala	Thr	Val	Ile	Val	Ile	Thr	Leu	Val	Met	Leu
	690					695					700				
Lys	Lys	Lys	Gln	Tyr	Thr	Ser	Ile	His	His	Gly	Val	Val	Glu	Val	Asp
705					710					715					720
Ala	Ala	Val	Thr	Pro	Glu	Glu	Arg	His	Leu	Ser	Lys	Met	Gln	Gln	Asn
				725					730					735	
Gly	Tyr	Glu	Asn	Pro	Thr	Tyr	Lys	Phe	Phe	Glu	Gln	Met	Gln	Asn	
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 <211> 2316  
 <212> DNA  
 <213> Homo sapiens

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 ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaa 180  
 acctgcattg ataccaagga aggcacctcg cagtattgcc aagaagtcta ccctgaactg 240  
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 ggccgcaagc agtgcaagac ccacccccac tttgtgatc cctaccgctg cttagttagt 360  
 gagtttgtaa gtgatgcct tctcgttcct gacaagtgca aattcttaca ccaggagagg 420  
 atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagttag 480  
 aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga 540  
 ggggtagagt ttgtgtgttg cccactgyct gaagaaagtg acaatgtgga ttctgctgat 600  
 gcggaggagg atgactcggg tgtctgggtg ggcggagcag acacagacta tgcagatggg 660  
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 gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780  
 ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840  
 gagtctgtgg aagaggtggt tcgagaggtg tgctctgaac aagccgagac ggggccgtgc 900  
 cgagcaatga tctcccgctg gtactttgat gtgactgaag ggaagtgtgc cccattcttt 960  
 tacggcggat gtggcgccaa ccggaacaac tttgacacag aagagtactg catggccgtg 1020  
 tgtggcagcg ccatgtccca aagtttactc aagactaccg aggaacctct tggccgagat 1080  
 cctgttaaac ttccctacaac agcagccagt acccctgatg ccgttgacaa gtatctcyag 1140  
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 aagcaccgag agagaatgtc ccaggtcatg agagaatggg aagaggcaga acgtcaagca 1260  
 aagaacttgc ctaaagctga taagaaggca gttatccagc atttccagga gaaagtggaa 1320  
 tctttggaac aggaagcagc caacgagaga cagcagctgg tggagacaca catggccaga 1380  
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 gaacagaagg acagacagca caccctaaag catttgcgagc atgtgcgcat ggtggatccc 1560  
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 acctacaagt tctttgagca gatgcagaac aagaag 2316

<210> 59  
 <211> 772  
 <212> PRT  
 <213> Homo sapiens

<400> 59  
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 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
 35 40 45

Asn	Gly	Lys	Trp	Asp	Ser	Asp	Pro	Ser	Gly	Thr	Lys	Thr	Cys	Ile	Asp
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Thr	Lys	Glu	Gly	Ile	Leu	Gln	Tyr	Cys	Gln	Glu	Val	Tyr	Pro	Glu	Leu
65					70					75					80
Gln	Ile	Thr	Asn	Val	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn
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Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val
			100					105					110		
Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu
		115					120					125			
Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys
		130				135					140				
Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu
145					150					155					160
Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile
				165					170					175	
Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu
			180					185					190		
Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val
		195					200					205			
Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys
	210					215					220				
Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu
225					230					235					240
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu
				245					250					255	
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile
			260					265					270		
Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg
		275					280					285			
Glu	Val	Cys	Ser	Glu	Gln	Ala	Glu	Thr	Gly	Pro	Cys	Arg	Ala	Met	Ile
	290					295					300				
Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe
305					310					315					320
Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Asn	Phe	Asp	Thr	Glu	Glu	Tyr
				325					330					335	
Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Met	Ser	Gln	Ser	Leu	Leu	Lys	Thr
			340					345					350		
Thr	Gln	Glu	Pro	Leu	Ala	Arg	Asp	Pro	Val	Lys	Leu	Pro	Thr	Thr	Ala
		355					360					365			
Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp
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<210> 61
<211> 753
<212> PRT
<213> Homo sapiens
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Gln	Ile	Ala 35	Met	Phe	Cys	Gly	Arg 40	Leu	Asn	Met	His	Met 45	Asn	Val	Gln
Asn	Gly 50	Lys	Trp	Asp	Ser	Asp 55	Pro	Ser	Gly	Thr	Lys 60	Thr	Cys	Ile	Asp
Thr 65	Lys	Glu	Gly	Ile	Leu 70	Gln	Tyr	Cys	Gln	Glu	Val 75	Tyr	Pro	Glu	Leu 80
Gln	Ile	Thr	Asn	Val 85	Val	Glu	Ala	Asn	Gln 90	Pro	Val	Thr	Ile	Gln 95	Asn
Trp	Cys	Lys	Arg 100	Gly	Arg	Lys	Gln	Cys 105	Lys	Thr	His	Pro	His 110	Phe	Val
Ile	Pro	Tyr 115	Arg	Cys	Leu	Val	Gly 120	Glu	Phe	Val	Ser	Asp 125	Ala	Leu	Leu
Val 130	Pro	Asp	Lys	Cys	Lys	Phe 135	Leu	His	Gln	Glu	Arg 140	Met	Asp	Val	Cys
Glu 145	Thr	His	Leu	His	Trp 150	His	Thr	Val	Ala	Lys 155	Glu	Thr	Cys	Ser	Glu 160
Lys	Ser	Thr	Asn	Leu 165	His	Asp	Tyr	Gly 170	Met	Leu	Leu	Pro	Cys	Gly 175	Ile
Asp	Lys	Phe	Arg 180	Gly	Val	Glu	Phe	Val 185	Cys	Cys	Pro	Leu	Ala 190	Glu	Glu
Ser	Asp	Asn 195	Val	Asp	Ser	Ala	Asp 200	Ala	Glu	Glu	Asp 205	Asp	Ser	Asp	Val
Trp 210	Trp	Gly	Gly	Ala	Asp	Thr 215	Asp	Tyr	Ala	Asp 220	Gly	Ser	Glu	Asp	Lys
Val 225	Val	Glu	Val	Ala	Glu 230	Glu	Glu	Glu	Val	Ala 235	Glu	Val	Glu	Glu	Glu 240
Glu	Ala	Asp	Asp	Asp 245	Glu	Asp	Asp	Glu	Asp 250	Gly	Asp	Glu	Val	Glu 255	Glu
Glu	Ala	Glu	Glu 260	Pro	Tyr	Glu	Glu	Ala 265	Thr	Glu	Arg	Thr	Thr 270	Ser	Ile
Ala	Thr	Thr 275	Thr	Thr	Thr	Thr	Thr 280	Glu	Ser	Val	Glu 285	Glu	Val	Val	Arg
Glu 290	Val	Cys	Ser	Glu	Gln	Ala 295	Glu	Thr	Gly	Pro	Cys 300	Arg	Ala	Met	Ile
Ser 305	Arg	Trp	Tyr	Phe	Asp 310	Val	Thr	Glu	Gly	Lys 315	Cys	Ala	Pro	Phe	Phe 320

Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Asn	Phe	Asp	Thr	Glu	Glu	Tyr
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Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Ile	Pro	Thr	Thr	Ala	Ala	Ser	Thr
			340					345					350		
Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp	Glu	Asn	Glu
		355					360					365			
His	Ala	His	Phe	Gln	Lys	Ala	Lys	Glu	Arg	Leu	Glu	Ala	Lys	His	Arg
	370					375					380				
Glu	Arg	Met	Ser	Gln	Val	Met	Arg	Glu	Trp	Glu	Glu	Ala	Glu	Arg	Gln
385				390						395					400
Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	Lys	Lys	Ala	Val	Ile	Gln	His	Phe
			405						410					415	
Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	Gln	Glu	Ala	Ala	Asn	Glu	Arg	Gln
			420					425					430		
Gln	Leu	Val	Glu	Thr	His	Met	Ala	Arg	Val	Glu	Ala	Met	Leu	Asn	Asp
	435					440						445			
Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	Tyr	Ile	Thr	Ala	Leu	Gln	Ala	Val
	450					455					460				
Pro	Pro	Arg	Pro	Arg	His	Val	Phe	Asn	Met	Leu	Lys	Lys	Tyr	Val	Arg
465					470					475					480
Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	Thr	Leu	Lys	His	Phe	Glu	His	Val
				485					490					495	
Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	Ala	Gln	Ile	Arg	Ser	Gln	Val	Met
			500					505					510		
Thr	His	Leu	Arg	Val	Ile	Tyr	Glu	Arg	Met	Asn	Gln	Ser	Leu	Ser	Leu
	515						520						525		
Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala	Glu	Glu	Ile	Gln	Asp	Glu	Val	Asp
	530					535					540				
Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn	Tyr	Ser	Asp	Asp	Val	Leu	Ala	Asn
545					550					555					560
Met	Ile	Ser	Glu	Pro	Arg	Ile	Ser	Tyr	Gly	Asn	Asp	Ala	Leu	Met	Pro
				565					570					575	
Ser	Leu	Thr	Glu	Thr	Lys	Thr	Thr	Val	Glu	Leu	Leu	Pro	Val	Asn	Gly
			580					585					590		
Glu	Phe	Ser	Leu	Asp	Asp	Leu	Gln	Pro	Trp	His	Ser	Phe	Gly	Ala	Asp
	595						600					605			
Ser	Val	Pro	Ala	Asn	Thr	Glu	Asn	Glu	Val	Glu	Pro	Val	Asp	Ala	Arg
	610					615					620				
Pro	Ala	Ala	Asp	Arg	Gly	Leu	Thr	Thr	Arg	Pro	Gly	Ser	Gly	Leu	Thr
625					630					635					640
Asn	Ile	Lys	Thr	Glu	Glu	Ile	Ser	Glu	Val	Lys	Met	Asp	Ala	Glu	Phe
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<210> 67
<211> 475
<212> PRT
<213> Homo sapiens .
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 Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly  
 35 40 45  
 Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu  
 50 55 60  
 Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met  
 65 70 75 80  
 Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met  
 85 90 95  
 Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly  
 100 105 110  
 Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr  
 115 120 125  
 Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp  
 130 135 140  
 Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu  
 145 150 155 160  
 Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn  
 165 170 175  
 Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys  
 180 185 190  
 Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser  
 195 200 205  
 Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile  
 210 215 220  
 Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala  
 225 230 235 240  
 Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro  
 245 250 255  
 Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp  
 260 265 270  
 Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu  
 275 280 285  
 Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser  
 290 295 300  
 Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val  
 305 310 315 320  
 Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe  
 325 330 335  
 Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp  
 340 345 350

095644 050204

Asn Ile Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro  
165 170 175

Val Ala Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile  
180 185 190

Glu Pro Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu  
195 200 205

Glu Trp Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln  
210 215 220

Ser Leu Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val  
225 230 235 240

Asp Ser Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala  
245 250 255

Val Val Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp  
260 265 270

Gly Phe Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr  
275 280 285

Pro Trp Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn  
290 295 300

Ser Ser Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln  
305 310 315 320

Pro Met Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile  
325 330 335

Ser Pro Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly  
340 345 350

Phe Tyr Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala  
355 360 365

Ser Pro Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly  
370 375 380

Pro Phe Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser  
385 390 395 400

Leu Ser Glu Pro Ile Leu Trp His His His His His His  
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<210> 69

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

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Gly Leu Ala Leu Ala Leu Glu Pro

1

5

<210> 70

<211> 8

<212> PRT

<213> Artificial Sequence

006634 0004  
100250 4225950

<220>

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<210> 80
<211> 15
<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Peptide

Met Cys Ala Glu Val Lys Met Asp Ala Glu Phe Lys Asp Asn Pro  
1 5 10 15

<211> 5

&lt;212&gt; PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: synthetic

Asp Ala Glu Phe Arg  
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<211> 5

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: synthetic

Ser Glu Val Asn Leu  
1 - - - - - 5